

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/900,425

DATE: 11/06/2001
TIME: 12:06:37

Input Set : A:\ispbh522.txt
Output Set: N:\CRF3\11062001\I900425.raw

3 <110> APPLICANT: Wu, Hongjiang
 4 Crooke, Stanley T.
 6 <120> TITLE OF INVENTION: Human RNase III and Compositions and Uses Thereof
 8 <130> FILE REFERENCE: ISPH-0522
 W--> 9 <140> CURRENT APPLICATION NUMBER: US 09/900,425
 10 <141> CURRENT FILING DATE: 2001-07-06
 12 <150> PRIOR APPLICATION NUMBER: US 09/479,783
 13 <151> PRIOR FILING DATE: 2000-01-07
 15 <150> PRIOR APPLICATION NUMBER: US 08/870,608
 16 <151> PRIOR FILING DATE: 1997-06-06
 18 <150> PRIOR APPLICATION NUMBER: US 80/659,440
 19 <151> PRIOR FILING DATE: 1996-06-06
 21 <160> NUMBER OF SEQ ID NOS: 36
 23 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

192 <210> SEQ ID NO: 2
 193 <211> LENGTH: 1374
 194 <212> TYPE: PRT
 195 <213> ORGANISM: Homo sapiens
 197 <400> SEQUENCE: 2
 199 Met Met Gln Gly Asn Thr Cys His Arg Met Ser Phe His Pro Gly Arg
 200 1 5 10 15
 202 Gly Cys Pro Arg Gly Arg Gly Gly His Gly Ala Arg Pro Ser Ala Pro
 203 20 25 30
 205 Ser Phe Arg Pro Gln Asn Leu Arg Leu Leu His Pro Gln Gln Pro Pro
 206 35 40 45
 208 Val Gln Tyr Gln Tyr Glu Pro Pro Ser Ala Pro Ser Thr Thr Phe Ser
 209 50 55 60
 211 Asn Ser Pro Ala Pro Asn Phe Leu Pro Pro Arg Pro Asp Phe Val Pro
 212 65 70 75 80
 214 Phe Pro Pro Pro Met Pro Pro Ser Ala Gln Gly Pro Leu Pro Pro Cys
 215 85 90 95
 217 Pro Ile Arg Pro Pro Phe Pro Asn His Gln Met Arg His Pro Phe Pro
 218 100 105 110
 220 Val Pro Pro Cys Phe Pro Pro Met Pro Pro Pro Met Pro Cys Pro Asn
 221 115 120 125
 223 Asn Pro Pro Val Pro Gly Ala Pro Pro Gly Gln Gly Thr Phe Pro Phe
 224 130 135 140
 226 Met Met Pro Pro Pro Ser Met Pro His Pro Pro Pro Pro Val Met
 227 145 150 155 160
 229 Pro Gln Gln Val Asn Tyr Gln Tyr Pro Pro Gly Tyr Ser His His Asn
 230 165 170 175
 232 Phe Pro Pro Pro Ser Phe Asn Ser Phe Gln Asn Asn Pro Ser Ser Phe
 233 180 185 190

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235 Leu Pro Ser Ala Asn Asn Ser Ser Ser Pro His Phe Arg His Leu Pro
 236 195 200 205
 238 Pro Tyr Pro Leu Pro Lys Ala Pro Ser Glu Arg Arg Ser Pro Glu Arg
 239 210 215 220
 241 Leu Lys His Tyr Asp Asp His Arg His Arg Asp His Ser His Gly Arg
 242 225 230 235 240
 244 Gly Glu Arg His Arg Ser Leu Asp Arg Arg Glu Arg Gly Arg Ser Pro
 245 245 250 255
 247 Asp Arg Arg Arg Gln Asp Ser Arg Tyr Arg Ser Asp Tyr Asp Arg Gly
 248 260 265 270
 250 Arg Thr Pro Ser Arg His Arg Ser Tyr Glu Arg Ser Arg Glu Arg Glu
 251 275 280 285
 253 Arg Glu Arg His Arg His Arg Asp Asn Arg Arg Ser Pro Ser Leu Glu
 254 290 295 300
 256 Arg Ser Tyr Lys Lys Glu Tyr Lys Arg Ser Gly Arg Ser Tyr Gly Leu
 257 305 310 315 320
 259 Ser Val Val Pro Glu Pro Ala Gly Cys Thr Pro Glu Leu Pro Gly Glu
 260 325 330 335
 262 Ile Ile Lys Asn Thr Asp Ser Trp Ala Pro Pro Leu Glu Ile Val Asn
 263 340 345 350
 265 His Arg Ser Pro Ser Arg Glu Lys Lys Arg Ala Arg Trp Glu Glu Glu
 266 355 360 365
 268 Lys Asp Arg Trp Ser Asp Asn Gln Ser Ser Gly Lys Asp Lys Asn Tyr
 269 370 375 380
 271 Thr Ser Ile Lys Glu Lys Glu Pro Glu Glu Thr Met Pro Asp Lys Asn
 272 385 390 395 400
 274 Glu Glu Glu Glu Glu Leu Leu Lys Pro Val Trp Ile Arg Cys Thr
 275 405 410 415
 277 His Ser Glu Asn Tyr Tyr Ser Ser Asp Pro Met Asp Gln Val Gly Asp
 278 420 425 430
 280 Ser Thr Val Val Gly Thr Ser Arg Leu Arg Asp Leu Tyr Asp Lys Phe
 281 435 440 445
 283 Glu Glu Glu Leu Gly Ser Arg Gln Glu Lys Ala Lys Ala Ala Arg Pro
 284 450 455 460
 286 Pro Trp Glu Pro Pro Lys Thr Lys Leu Asp Glu Asp Leu Glu Ser Ser
 287 465 470 475 480
 289 Ser Glu Ser Glu Cys Glu Ser Asp Glu Asp Ser Thr Cys Ser Ser Ser
 290 485 490 495
 292 Ser Asp Ser Glu Val Phe Asp Val Ile Ala Glu Ile Lys Arg Lys Lys
 293 500 505 510
 295 Ala His Pro Asp Arg Leu His Asp Glu Leu Trp Tyr Asn Asp Pro Gly
 296 515 520 525
 298 Gln Met Asn Asp Gly Pro Leu Cys Lys Cys Ser Ala Lys Ala Arg Arg
 299 530 535 540
 301 Thr Gly Ile Arg His Ser Ile Tyr Pro Gly Glu Glu Ala Ile Lys Pro
 302 545 550 555 560
 304 Cys Arg Pro Met Thr Asn Asn Ala Gly Arg Leu Phe His Tyr Arg Ile
 305 565 570 575
 307 Thr Val Ser Pro Pro Thr Asn Phe Leu Thr Asp Arg Pro Thr Val Ile

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308	580	585	590
310	Glu Tyr Asp Asp His Glu Tyr Ile Phe Glu Gly Phe Ser Met Phe Ala		
311	595	600	605
313	His Ala Pro Leu Thr Asn Ile Pro Leu Cys Lys Val Ile Arg Phe Asn		
314	610	615	620
316	Ile Asp Tyr Thr Ile His Phe Ile Glu Glu Met Met Pro Glu Asn Phe		
317	625	630	635
319	Cys Val Lys Gly Leu Glu Leu Phe Ser Leu Phe Leu Phe Arg Asp Ile		
320	645	650	655
322	Leu Glu Leu Tyr Asp Trp Asn Leu Lys Gly Pro Leu Phe Glu Asp Ser		
323	660	665	670
325	Pro Pro Cys Cys Pro Arg Phe His Phe Met Pro Arg Phe Val Arg Phe		
326	675	680	685
328	Leu Pro Asp Gly Gly Lys Glu Val Leu Ser Met His Gln Ile Leu Leu		
329	690	695	700
331	Tyr Leu Leu Arg Cys Ser Lys Ala Leu Val Pro Glu Glu Glu Ile Ala		
332	705	710	715
334	Asn Met Leu Gln Trp Glu Glu Leu Glu Trp Gln Lys Tyr Ala Glu Glu		
335	725	730	735
337	Cys Lys Gly Met Ile Val Thr Asn Pro Gly Thr Lys Pro Ser Ser Val		
338	740	745	750
340	Arg Ile Asp Gln Leu Asp Arg Glu Gln Phe Asn Pro Asp Val Ile Thr		
341	755	760	765
343	Phe Pro Ile Ile Val His Phe Gly Ile Arg Pro Ala Gln Leu Ser Tyr		
344	770	775	780
346	Ala Gly Asp Pro Gln Tyr Gln Lys Leu Trp Lys Ser Tyr Val Lys Leu		
347	785	790	795
349	Arg His Leu Leu Ala Asn Ser Pro Lys Val Lys Gln Thr Asp Lys Gln		
350	805	810	815
352	Lys Leu Ala Gln Arg Glu Glu Ala Leu Gln Lys Ile Arg Gln Lys Asn		
353	820	825	830
355	Thr Met Arg Arg Glu Val Thr Val Glu Leu Ser Ser Gln Gly Phe Trp		
356	835	840	845
358	Lys Thr Gly Ile Arg Ser Asp Val Cys Gln His Ala Met Met Leu Pro		
359	850	855	860
361	Val Leu Thr His His Ile Arg Tyr His Gln Cys Leu Met His Leu Asp		
362	865	870	875
364	Lys Leu Ile Gly Tyr Thr Phe Gln Asp Arg Cys Leu Leu Gln Leu Ala		
365	885	890	895
367	Met Thr His Pro Ser His His Leu Asn Phe Gly Met Asn Pro Asp His		
368	900	905	910
370	Ala Arg Asn Ser Leu Ser Asn Cys Gly Ile Arg Gln Pro Lys Tyr Gly		
371	915	920	925
373	Asp Arg Lys Val His His Met His Arg Lys Lys Gly Ile Asn Thr		
374	930	935	940
376	Leu Ile Asn Ile Met Ser Arg Leu Gly Gln Asp Asp Pro Thr Pro Ser		
377	945	950	955
379	Arg Ile Asn His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ala Val Val		
380	965	970	975

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382 Glu Phe Leu Thr Ser Val His Leu Tyr Tyr Leu Phe Pro Ser Leu Glu
 383 980 985 990
 385 Glu Gly Gly Leu Ala Thr Tyr Arg Thr Ala Ile Val Gln Asn Gln His
 386 995 1000 1005
 388 Leu Ala Met Leu Ala Lys Lys Leu Glu Leu Asp Pro Phe Met Leu Tyr
 389 1010 1015 1020
 391 Ala His Gly Pro Asp Leu Cys Arg Glu Ser Asp Leu Arg His Ala Met
 392 1025 1030 1035 1040
 394 Ala Asn Cys Phe Glu Ala Leu Ile Gly Ala Val Tyr Leu Glu Gly Ser
 395 1045 1050 1055
 397 Leu Glu Glu Ala Lys Gln Leu Phe Gly Arg Leu Leu Phe Asn Asp Pro
 398 1060 1065 1070
 400 Asp Leu Arg Glu Val Trp Leu Asn Tyr Pro Leu His Pro Leu Gln Leu
 401 1075 1080 1085
 403 Gln Glu Pro Asn Thr Asp Arg Gln Leu Ile Glu Thr Ser Pro Val Leu
 404 1090 1095 1100
 406 Gln Lys Leu Thr Glu Phe Glu Glu Ala Ile Gly Val Ile Phe Thr His
 407 1105 1110 1115 1120
 409 Val Arg Leu Leu Ala Arg Ala Phe Thr Leu Arg Thr Val Gly Phe Asn
 410 1125 1130 1135
 412 His Leu Thr Leu Gly His Asn Gln Arg Met Glu Phe Leu Gly Asp Ser
 413 1140 1145 1150
 415 Ile Met Gln Leu Val Ala Thr Glu Tyr Leu Phe Ile His Phe Pro Asp
 416 1155 1160 1165
 418 His His Glu Gly His Leu Thr Leu Leu Arg Ser Ser Leu Val Asn Asn
 419 1170 1175 1180
 421 Arg Thr Gln Ala Lys Val Ala Glu Glu Leu Gly Met Gln Glu Tyr Ala
 422 1185 1190 1195 1200
 424 Ile Thr Asn Asp Lys Thr Lys Arg Pro Val Gly Leu Arg Thr Lys Thr
 425 1205 1210 1215
 427 Leu Ala Asp Leu Leu Glu Ser Phe Ile Ala Ala Leu Tyr Thr Asp Lys
 428 1220 1225 1230
 430 Asp Leu Glu Tyr Val His Thr Phe Met Asn Val Cys Phe Phe Pro Arg
E--> 431 1235 1240 1245
 433 Leu Lys Glu Phe Ile Leu Asn Gln Asp Trp Asn Asp Pro Lys Ser Gln
E--> 434 1250 1255 1260 1265
 436 Leu Gln Gln Cys Cys Leu Thr Leu Arg Thr Glu Gly Lys Glu Pro Asp
E--> 437 1270 1275 1280
 439 Ile Pro Leu Tyr Lys Thr Leu Gln Thr Val Gly Pro Ser His Ala Arg
E--> 440 1285 1290 1295
 442 Thr Tyr Thr Val Ala Val Tyr Phe Lys Gly Glu Arg Ile Gly Cys Gly
E--> 443 1300 1305 1310
 445 Lys Gly Pro Ser Ile Gln Gln Ala Glu Met Gly Ala Ala Met Asp Ala
E--> 446 1315 1320 1325
 448 Leu Glu Lys Tyr Asn Phe Pro Gln Met Ala His Gln Lys Arg Phe Ile
E--> 449 1330 1335 1340 1345
 451 Gly Arg Lys Tyr Arg Gln Glu Leu Lys Glu Met Arg Trp Glu Arg Glu
E--> 452 1350 1355 1360
 455 His Gln Glu Arg Glu Pro Asp Glu Thr Glu Asp Ile Lys Lys

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Input Set : A:\isph522.txt
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E--> 456 1365 1370 *error along seqt*
1095 <210> SEQ ID NO: 36
1096 <211> LENGTH: 20
1097 <212> TYPE: PRT
1098 <213> ORGANISM: Homo sapiens
1100 <400> SEQUENCE: 36
1102 Cys Arg Trp Glu Arg Glu His Gln Glu Arg Glu Pro Asp Glu Thr Glu
1103 1 5 10 15
1105 Asp Ile Lys Lys
1106 20

E--> 1109 19
E--> 1112 19
E--> 1115 1
E--> 1118 2
delete seqt

VERIFICATION SUMMARY DATE: 11/06/2001
PATENT APPLICATION: US/09/900,425 TIME: 12:06:38

Input Set : A:\ispbh522.txt
Output Set: N:\CRF3\11062001\I900425.raw

L:9 M:283 W: Missing Blank Line separator, <140> field identifier
L:431 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:787 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:788 M:283 W: Missing Blank Line separator, <220> field identifier
L:798 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:799 M:283 W: Missing Blank Line separator, <220> field identifier
L:809 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:810 M:283 W: Missing Blank Line separator, <220> field identifier
L:820 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:821 M:283 W: Missing Blank Line separator, <220> field identifier
L:831 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:832 M:283 W: Missing Blank Line separator, <220> field identifier
L:842 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:843 M:283 W: Missing Blank Line separator, <220> field identifier
L:853 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:854 M:283 W: Missing Blank Line separator, <220> field identifier
L:864 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:865 M:283 W: Missing Blank Line separator, <220> field identifier
L:875 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:876 M:283 W: Missing Blank Line separator, <220> field identifier
L:885 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:897 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:898 M:283 W: Missing Blank Line separator, <220> field identifier
L:908 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:909 M:283 W: Missing Blank Line separator, <220> field identifier
L:919 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:920 M:283 W: Missing Blank Line separator, <220> field identifier
L:930 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:931 M:283 W: Missing Blank Line separator, <220> field identifier
L:941 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:942 M:283 W: Missing Blank Line separator, <220> field identifier
L:952 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:953 M:283 W: Missing Blank Line separator, <220> field identifier
L:963 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:964 M:283 W: Missing Blank Line separator, <220> field identifier
L:974 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:975 M:283 W: Missing Blank Line separator, <220> field identifier
L:985 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:986 M:283 W: Missing Blank Line separator, <220> field identifier
L:996 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
L:997 M:283 W: Missing Blank Line separator, <220> field identifier
L:1007 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28
L:1008 M:283 W: Missing Blank Line separator, <220> field identifier
L:1018 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
L:1019 M:283 W: Missing Blank Line separator, <220> field identifier
L:1029 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30
L:1030 M:283 W: Missing Blank Line separator, <220> field identifier

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Input Set : A:\isph522.txt
Output Set: N:\CRF3\11062001\I900425.raw

L:1040 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31
L:1041 M:283 W: Missing Blank Line separator, <220> field identifier
L:1051 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32
L:1052 M:283 W: Missing Blank Line separator, <220> field identifier
L:1062 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33
L:1063 M:283 W: Missing Blank Line separator, <220> field identifier
L:1073 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34
L:1074 M:283 W: Missing Blank Line separator, <220> field identifier
L:1109 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
M:332 Repeated in SeqNo=36

STATISTICS SUMMARY

PATENT APPLICATION: US/09/900,425

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Input Set : A:\isph522.txt

Output Set: N:\CRF3\11062001\I900425.raw

Application Serial Number: US/09/900,425

Alpha or Numeric: Numeric

Application Class:

Application File Date: 07-06-2001

Art Unit: OIPE

Software Application: PatentIn

Total Number of Sequences: 36

Total Nucleotides: 5531

Total Amino Acids: 2900

Number of Errors: 13

Number of Warnings: 27

Number of Corrections: 27

MESSAGE SUMMARY

220 C: 27 (Keyword misspelled or invalid format)

283 W: 27 (Missing Blank Line separator)

332 E: 13 ((32) Invalid/Missing Amino Acid Numbering)